

Phase Unwrapping of PCMRI data

J. B. Drexl¹, O. Friman², A. Hennemuth², J. Bock³, M. Markl³, and H. K. Hahn¹

¹Fraunhofer MEVIS, Bremen, Bremen, Germany, ²Fraunhofer MEVIS, ³Department of Radiology, Medical Physics, University Hospital Freiburg, Germany

ABSTRACT Phase contrast magnetic resonance imaging (PCMRI) utilizes the effect of a bipolar gradient pair on moving spins to encode velocity into the phase of the MR signal, so that the phase is linearly proportional to velocity of the spins [3]. The velocity can be recovered by taking the argument $\arg(S)$ of the measured complex signal, which, however, gives the phase modulus 2π . Spins moving faster than a pre-selected VENC factor will therefore be aliased or wrapped to an erroneous value. The amount of phase wrapping can be minimized by choosing a higher VENC, but this reduces the measurement range and increases noise, and a phase-unwrapping step is therefore standard in PCMRI analysis. In this work, the PRELUDE phase unwrapping method [2] is evaluated for PCMRI analysis. Furthermore, the effects of 2D slicewise versus full 3D unwrapping are investigated.

PHASE UNWRAPPING Among the best known state-of-the-art generic methods for phase unwrapping are path following algorithms (e.g. Goldstein, Flynn) [1], Minimum-Norm methods [1] and general energy based methods (e.g. based on Markov Random Fields).

An interesting energy-based method is Jenkinson's PRELUDE algorithm. It has been specifically designed for MRI (although not for PCMRI flow data), is able to work in 3D as well as in 2D and is fast for data with low SNR [2]. PRELUDE decomposes the wrapped phase image into piecewise-constant-regions. In such a region no phase wrapping is assumed to occur, so in a region A the unwrapped phase u will be related to the wrapped phase w by $u_A = w_A + 2\pi M_A$, where M_A is an integer offset ("wrap count") common to all pixels in region A.

The unwrapping problem is recast as the optimization of a cost function penalizing the sum of squared differences in phase between two regions A and B:

$$C_{AB} = \sum_{j \in A} \sum_{k \in N(j) \cap B} (w_j - w_k + 2\pi(M_A - M_B))^2.$$

PRELUDE computes wrap counts M_A for each region by minimizing the total cost over all region pairs AB by doing a greedy search.

For PCMRI flow data of the aorta we want to mask out at least air-filled regions like background and lungs. These regions have low SNR, so the phase information is locally very unstable. We use the default mask generation algorithm of PRELUDE: Automatically compute a threshold based on the 2% and 98% quantiles of the greyvalue histogram of the magnitude image, threshold and retain the biggest connected component.

MATERIAL We acquired 4D PCI MRI data of the aorta of a volunteer on a Siemens TrioTim scanner (3 Tesla), employing three different VENCs. The parameters were spatiotemporal resolution = $1.6 \times 2.1 \times 2.3 \text{ mm}^3 \times 42.4 \text{ ms}$, TE/TR = 2.711/5.3, flip angle 7° . VENCs employed were 40cm/s, 100cm/s, and 150 cm/s. No further preprocessing like eddy current correction etc was performed. The 150 cm/s contain only very few wraps. The 100 cm/s show large wrapped areas, and sometimes even double wraps. The 40cm/s contain vast wrapped areas, with sometimes up to quadruple wraps.

RESULTS FOR THE REAL DATASETS We ran PRELUDE on all three VENCs, in full 3D as well as in slicewise 2D mode. By visual inspection we found all automatically generated masks for background removal to be of good quality. They effectively mask out the air-filled areas without damaging the aorta region. In both 2D slicewise as well as in full 3D mode we find that the unwrapping results for 150 cm/s and 100 cm/s are very good. PRELUDE is able to unwrap all phase wraps present in the datasets. For the 40 cm/s dataset we see that some phase wraps are unwrapped, but the overall quality is still insufficient. Also by visual inspection, it is not possible to judge either the 2D slicewise or the full 3D mode of a higher overall quality. For the processing times on a Intel 2 Quad Processor machine running at 2.4 Ghz with 4 GB main memory we measure the following processing times:

| | 40 cm/sec | 100 cm/sec | 150 cm/sec |
|--------------|-----------|------------|------------|
| Full 3D | 150 min | 283 sec | 223 sec |
| Slicewise 2D | 563 sec | 155 sec | 163 sec |

DIGITAL PHANTOM To further explore the quality difference between 2D slicewise and full 3D, we constructed a digital phantom. Although the three scans are from the same volunteer, they show temporal displacement. Thus, they do not possess a strict voxel-to-voxel-correspondance, which makes it impossible to use one of them as gold standard. To deal with this problem, we decided to construct a digital phantom:

- unwrap venc 150 and check that no more wraps are present. This dataset now is designated the ground truth.

- Re-scale the data to VENC=100 cm/s and re-wrap. We checked the realism of the phantom by manually comparing the surrogate dataset to the real 100 cm/s dataset.

We use the misclassification rate as a metric for comparing a ground truth phase signal $s(k)$ to a reconstructed phase signal $u(k)$: $MCR = (1/N) \sum_k [s(k) \neq u(k)]$, with $[\cdot]$ denoting the Iverson bracket [2]. We ran PRELUDE on the phantom, in full 3D as well as in slicewise 2D mode. We obtain for the misclassification rates:

| | X component | Y component | Z component | Mean |
|--------------|-------------|-------------|-------------|---------|
| Full 3D | 1.05% | 0.94% | 0.35% | 0.7800% |
| Slicewise 2D | 1.06% | 0.95% | 0.35% | 0.7867% |

We conclude that by quantitative means, it is not possible here to judge either the 2D slicewise or the full 3D mode of a higher overall quality.

DISCUSSION PRELUDE is able to unwrap PCMRI data when the VENC is not too low. We cannot make a preference between 2D slicewise and full 3D based on a quality criteria. Because of its faster processing, we prefer the 2D slicewise mode. The question is still open if temporal information would help in the 40 cm/s case.

REFERENCES [1] D.C. Ghiglia et al. *Two-Dimensional Phase Unwrapping*, Wiley (1998). [2] M. Jenkinson. *Mag. Res. In Medicine* 49:193-197(2003) (1998). [3] M. Bernstein et al. *Handbook of MRI Pulse Sequences*, Academic Press (2004).

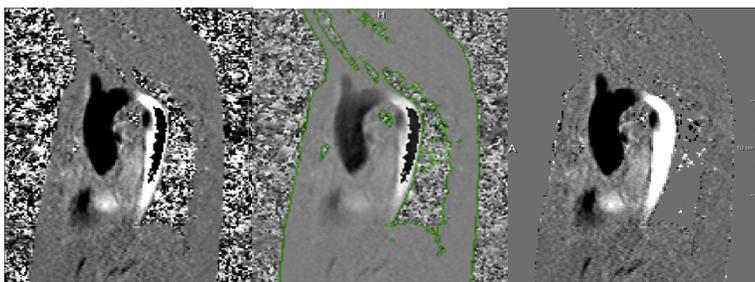


Fig 1. a) Slice from the 100 cm/s dataset b) with background mask. c) after unwrapping.

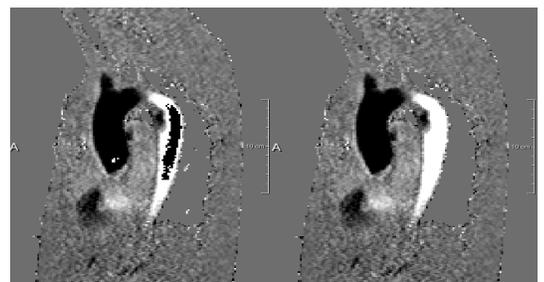


Fig 2.a) Phantom. b) after unwrapping.